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Supplemental Material

A Genome-Wide Analysis of DNA Methylation and Fine Particulate Matter Air Pollution in Three Study Populations: KORA F3, KORA F4, and the Normative Aging Study

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Figure S1. Forest plots for the eight CpG sites that showed Bonferroni genome-wide significance but results heterogeneous (I^2 p-value < 0.05 or $I^2 > 0.5$).

Figure S2. Residual plot for FDR significant CpG at 2-day average (F3=blue, F4=red, NAS=green).

Figure S3. Residual plot for FDR significant CpG at 7-day average (F3=blue, F4=red, NAS=green).

Figure S4. Residual plot for Bonferroni significant CpG at 28-day average (F3=blue, F4=red, NAS=green). For cg11046593, 21 methylation values were excluded and re-run the models and the meta-analysis. New p-value resulted 5.48E-08, still Bonferroni significant.

Table S1. Study specific regression coefficients of FDR (2- and 7-day average) and Bonferroni (28-day average) significant CpGs.

Table S2. Sensitivity analysis, comparison of fixed-effect regression coefficients (β) and p-values of fully-adjusted models in 28-day significant hits with and without yearly PM_{2.5} exposure adjustment.

Supplemental Code and Data Zip File

Excel File S1. FDR significant CpG sites for 28-day PM_{2.5}